APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/756,096	01/08/2001	Lloyd G. Mitchell	A31304-B-A-B	5647

21003   7590   09/26/2002

BAKER & BOTTS -
30 ROCKEFELLER PLAZA
NEW YORK, NY 10112

EXAMINER
LACOURCIERE, KAREN A

ART UNIT	PAPER NUMBER
1635	

DATE MAILED: 09/26/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

Please find below and/or attached an Office communication concerning the above identified application.

Commissioner of Patents and Trademarks

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. To be fully responsive to this letter, this application must comply with all of the requirements set forth in 37 CFR 1.821 through 1.825.

Applicant is given THIRTY DAYS from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen A. Lacourciere whose telephone number is (703) 308-7523. The examiner can normally be reached on Monday to Friday from 8:30 a.m. to 4:30 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John LeGuyader, can be reached on (703) 308-0447. The fax phone number for this Group is (703) 308-4242.
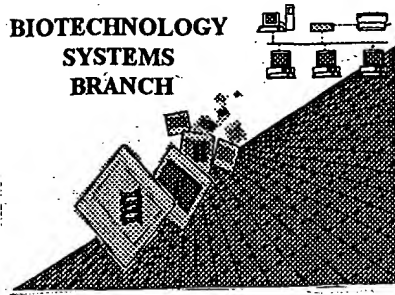
Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Karen A. Lacourciere
September 18, 2002

KAREN LACOURCIERE
PATENT EXAMINER

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/756,096_

Source: _OIPE_

Date Processed by STIC: _1/8/2002_

RECEIVED

MAY 2 2 2002

TECH CENTER 1600/2900

RECEIVED

APR 0 3 2002

OFFICE OF PETITIONS

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual - ePAVE**)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
             Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service,** r ther delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/756,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1 ___ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) 92 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 01/08/2002
PATENT APPLICATION: US/09/756,096   TIME: 15:21:15

Input Set : A:\09756096SEQUENCELISTING.txt
Output Set: N:\CRF3\01082002\I756096.raw

```
 4 <110> APPLICANT: Mitchell, Lloyd G.
 5        Garcia-Blanco, Mariano A.
 6        Puttaraju, Madaiah
 7        Mansfield, Gary S.
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
11        SPLICEOSOME MEDIATED RNA TRANS-SPLICING
14 <130> FILE REFERENCE: A31304-B-A-B 072874.0135
16 <140> CURRENT APPLICATION NUMBER: 09/756,096
17 <141> CURRENT FILING DATE: 2001-01-08
19 <150> PRIOR APPLICATION NUMBER: 09/158,863
20 <151> PRIOR FILING DATE: 1998-09-23
22 <150> PRIOR APPLICATION NUMBER: 09/133,717
23 <151> PRIOR FILING DATE: 1998-08-13
25 <150> PRIOR APPLICATION NUMBER: 09/087,233
26 <151> PRIOR FILING DATE: 1998-05-28
28 <150> PRIOR APPLICATION NUMBER: 08/766,354
29 <151> PRIOR FILING DATE: 1996-12-13
31 <150> PRIOR APPLICATION NUMBER: 60/008,317
32 <151> PRIOR FILING DATE: 1995-12-15
34 <160> NUMBER OF SEQ ID NOS: 105
36 <170> SOFTWARE: FastSEQ for Windows Version 4.0
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 132
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapien
43 <400> SEQUENCE: 1
44 caggggacgc accaaggatg gagatgttcc agggcgctga tgatgttgtt gattcttctt 60
45 aaatcttttg tgatggaaaa cttttcttcg taccacggga ctaaacctgg ttatgtagat 120
46 tccattcaaa aa                                                     132
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 29
50 <212> TYPE: DNA
51 <213> ORGANISM: Corynebacterium diptheriae
53 <400> SEQUENCE: 2
54 ggcgctgcag ggcgctgatg atgttgttg                                   29
56 <210> SEQ ID NO: 3
57 <211> LENGTH: 36
58 <212> TYPE: DNA
59 <213> ORGANISM: Corynebacterium diptheriae
61 <400> SEQUENCE: 3
62 ggcgaagctt ggatccgaca cgatttcctg cacagg                           36
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 68
66 <212> TYPE: DNA
67 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
70 <223> OTHER INFORMATION: Oligonucleotide
```

Does Not Comply
Corrected Diskette Needed

Input Set : A:\09756096SEQUENCELISTING.txt
Output Set: N:\CRF3\01082002\I756096.raw

```
 72 <400> SEQUENCE: 4
 73 aattctctag atgcttcacc cgggcctgac tcgagtacta actggtacct cttctttttt 60
 74 ttcctgca                                                         68
 76 <210> SEQ ID NO: 5
 77 <211> LENGTH: 60
 78 <212> TYPE: DNA
 79 <213> ORGANISM: Artificial Sequence
 81 <220> FEATURE:
 82 <223> OTHER INFORMATION: Oligonucleotide
 84 <400> SEQUENCE: 5
 85 ggaaaaaaaa gaagaggtac cagttagtac tcgagtcagg cccgggtgaa gcatctagag 60
 88 <210> SEQ ID NO: 6
 89 <211> LENGTH: 24
 90 <212> TYPE: DNA
 91 <213> ORGANISM: Artificial Sequence
 93 <220> FEATURE:
 94 <223> OTHER INFORMATION: Oligonucleotide primer
 96 <400> SEQUENCE: 6
 97 tcgagcaacg ttataataat gttc                                       24
 99 <210> SEQ ID NO: 7
100 <211> LENGTH: 24
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Oligonucleotide primer
107 <400> SEQUENCE: 7
108 tcgagaacat tattataacg ttgc                                       24
110 <210> SEQ ID NO: 8
111 <211> LENGTH: 35
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Oligonucleotide primer
118 <400> SEQUENCE: 8
119 aattctctag atcaggcccg ggtgaagcac tcgag                           35
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 25
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Oligonucleotide primer
129 <400> SEQUENCE: 9
130 tgcttcaccc gggcctgatc tagag                                      25
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 18
134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapien
137 <400> SEQUENCE: 10
138 tgcttcaccc gggcctga                                              18
```

Input Set : A:\09756096SEQUENCELISTING.txt
Output Set: N:\CRF3\01082002\I756096.raw

```
140 <210> SEQ ID NO: 11
141 <211> LENGTH: 16
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapien
145 <400> SEQUENCE: 11
146 ctcttctttt ttttcc                                            16
148 <210> SEQ ID NO: 12
149 <211> LENGTH: 18
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapien
153 <400> SEQUENCE: 12
154 caacgttata ataatgtt                                          18
156 <210> SEQ ID NO: 13
157 <211> LENGTH: 16
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapien
161 <400> SEQUENCE: 13
162 ctgtgattaa tagcgg                                            16
164 <210> SEQ ID NO: 14
165 <211> LENGTH: 16
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapien
169 <400> SEQUENCE: 14
170 cctggacgcg gaagtt                                            16
172 <210> SEQ ID NO: 15
173 <211> LENGTH: 51
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapien
177 <400> SEQUENCE: 15
178 ctgggacaag gacactgctt cacccggtta gtagaccaca gccctgaagc c       51
180 <210> SEQ ID NO: 16
181 <211> LENGTH: 17
182 <212> TYPE: DNA
183 <213> ORGANISM: Homo sapien
185 <400> SEQUENCE: 16
186 cttctgtttt ttttctc                                           17
188 <210> SEQ ID NO: 17
189 <211> LENGTH: 16
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapien
193 <400> SEQUENCE: 17
194 cttctgtatt attctc                                            16
196 <210> SEQ ID NO: 18
197 <211> LENGTH: 16
198 <212> TYPE: DNA
199 <213> ORGANISM: Homo sapien
201 <400> SEQUENCE: 18
202 gttctgtcct tgtctc                                            16
204 <210> SEQ ID NO: 19
```

RAW SEQUENCE LISTING   DATE: 01/08/2002
PATENT APPLICATION: US/09/756,096   TIME: 15:21:15

        Input Set : A:\09756096SEQUENCELISTING.txt
        Output Set: N:\CRF3\01082002\I756096.raw

205 <211> LENGTH: 29
206 <212> TYPE: DNA
207 <213> ORGANISM: Corynebacterium diptheriae
209 <400> SEQUENCE: 19
210 ggcgctgcag ggcgctgatg atgttgttg   29
212 <210> SEQ ID NO: 20
213 <211> LENGTH: 36
214 <212> TYPE: DNA
215 <213> ORGANISM: Corynebacterium diptheriae
217 <400> SEQUENCE: 20
218 ggcgaagctt ggatccgaca cgatttcctg cacagg   36
220 <210> SEQ ID NO: 21
221 <211> LENGTH: 21
222 <212> TYPE: DNA
223 <213> ORGANISM: Corynebacterium diptheriae
225 <400> SEQUENCE: 21
226 catcgtcata atttccttgt g   21
228 <210> SEQ ID NO: 22
229 <211> LENGTH: 20
230 <212> TYPE: DNA
231 <213> ORGANISM: Corynebacterium diptheriae
233 <400> SEQUENCE: 22
234 atggaatcta cataaccagg   20
236 <210> SEQ ID NO: 23
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Corynebacterium diptheriae
241 <400> SEQUENCE: 23
242 gaaggctgag cactacacgc   20
244 <210> SEQ ID NO: 24
245 <211> LENGTH: 20
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapien
249 <400> SEQUENCE: 24
250 cggcaccgtg gccgaagtgg   20
252 <210> SEQ ID NO: 25
253 <211> LENGTH: 30
254 <212> TYPE: DNA
255 <213> ORGANISM: Homo sapien
257 <400> SEQUENCE: 25
258 accggaattc atgaagccag gtacaccagg   30
260 <210> SEQ ID NO: 26
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Homo sapien
265 <400> SEQUENCE: 26
266 gggcaaggtg aacgtggatg   20
268 <210> SEQ ID NO: 27
269 <211> LENGTH: 19

Input Set : A:\09756096SEQUENCELISTING.txt
Output Set: N:\CRF3\01082002\I756096.raw

```
270 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapien
273 <400> SEQUENCE: 27
274 atcaggagtg gacagatcc                                            19
276 <210> SEQ ID NO: 28
277 <211> LENGTH: 39
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
282 <223> OTHER INFORMATION: Oligonucleotide primer complimentary to the
283       Escherichia coli lacZ gene
285 <400> SEQUENCE: 28
286 gcatgaattc ggtaccatgg gggggttctc atcatcatc                      39
288 <210> SEQ ID NO: 29
289 <211> LENGTH: 36
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: Oligonucleotide primer complimentary to the
295       Escherichia coli lacZ gene
297 <400> SEQUENCE: 29
298 ctgaggatcc tcttacctgt aaacgcccat actgac                         36
300 <210> SEQ ID NO: 30
301 <211> LENGTH: 38
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Oligonucleotide primer complimentary to the
307       Escherichia coli lacZ gene
309 <400> SEQUENCE: 30
310 gcatggtaac cctgcagggc ggcttcgtct gggactgg                       38
312 <210> SEQ ID NO: 31
313 <211> LENGTH: 38
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Oligonucleotide primer complimentary to the
319       Escherichia coli lacZ gene
321 <400> SEQUENCE: 31
322 ctgaaagctt gttaacttat tatttttgac accagacc                       38
324 <210> SEQ ID NO: 32
325 <211> LENGTH: 47
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Oligonucleotide primer complimentary to the
331       Escherichia coli lacZ gene
333 <400> SEQUENCE: 32
334 gcatggtaac cctgcagggc ggcttcgtct aataatggga ctgggtg             47
```

<210> 92
<211> 192
<212> DNA
<213> Artificial Sequence   *see item 11 on Error Summary Sheet*

<400> 92
```
acgagcttgc tcatgatgat catgggcgag ttagaaccaa gtgaaggcaa gatcaaacat 60
tccggccgca tcagcttttg cagccaattc agttggatca tgcccggtac catcaaggag 120
aacataatct tcggcgtcag ttacgacgag taccgctatc gctcggtgat taaggcctgt 180
cagttggagg ag                                                     192
```

FYI Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : **A:\09756096SEQUENCELISTING.txt**
Output Set: **N:\CRF3\01082002\I756096.raw**

L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
L:952 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
L:1030 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1030 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: